Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-11 (canceled):

Claim 12 (previously presented): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is a gene product whose activity or amount is reduced by an antisense nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1463, provided that cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claims 13-30 (canceled):

Claim 31 (previously presented): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising:

(a) providing a sublethal level of an antisense nucleic acid complementary to at least a portion of a nucleic acid encoding a gene product in a cell to reduce the activity or amount of said gene product in said cell, thereby producing a sensitized cell, wherein said gene product is selected from the group consisting of a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid of SEQ ID NO: 1463 a gene product having at least 25% amino acid

identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid of SEQ ID NO: 1463, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid selected of SEQ ID NO: 1463 under stringent conditions, a gene product encoded by a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleic acid comprising a nucleotide sequence of SEQ ID NO: 1463 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid of SEQ ID NO: 1463; provided that said cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits the growth of said sensitized cell relative to a nonsensitized cell.

Claims 32-44 (canceled):

Claim 45 (previously presented): The method of Claim 31, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 46 (previously presented): The method of Claim 31, wherein said gene product is from an organism other than *E. coli*.

Claim 47 (previously presented): The method of Claim 31, wherein said cell is an organism other than *E. coli*.

Claim 48 (previously presented): The method of Claim 31, wherein said sensitized cell is a pathogenic microorganism.

Claim 49 (previously presented): The method of Claim 31, wherein said sensitized cell is a Gram positive bacterium.

Claim 50 (previously presented): The method of Claim 49, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 51 (previously presented): The method of Claim 50, wherein said bacterium is *Staphylococcus aureus*.

Claim 52 (previously presented): The method of Claim 50, wherein said *Staphylococcus* species is coagulase negative.

Claim 53 (previously presented): The method of Claim 51, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 54 (previously presented): The method of Claim 31, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 55 (previously presented): The method of Claim 31, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 56 (previously presented): The method of Claim 31, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claim 57 (previously presented): The method of Claim 31, wherein said gene product is a polypeptide.

Claim 58 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 99% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600-and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 59 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 95% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 60 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 90% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 61 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 85% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 62 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 80% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 63 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 70% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 64 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 60% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 65 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 50% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 66 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 40% amino acid identity as determined using FASTA version 3.0t78 SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 67 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to SEQ ID NO: 12600 and a polypeptide whose activity may be complemented by a polypeptide of SEQ ID NO: 12600.

Claim 68 (previously presented): The method of Claim 57, wherein said polypeptide is 12600.

Claim 69 (previously presented): The method of Claim 57, wherein said polypeptide comprises a polypeptide selected from the group consisting of a polypeptide having at least 34% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 39% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600, a polypeptide having at least 42% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600 and a polypeptide having at least 43% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide having SEQ ID NO: 12600.

Claims 70-76 (canceled):

Claim 77 (Previously presented): The method of Claim 31, wherein said nucleic acid encoding said gene product is selected from the group consisting of SEQ ID NOs: 3966, 4228, 6154, 6592, 6872, 7273, 7857, 8502, 9420 and 9605.

Claim 78 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 97% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 79 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 95% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 80 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 90% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 81 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 85% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 82 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 80% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 83 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to SEQ ID NO: 1463.

Claim 84 (previously presented): The method of Claim 31, wherein said antisense nucleic acid comprises a nucleic acid having at least 70% nucleotide sequence identity to a nucleotide sequence comprising at least 100 consecutive nucleotides of SEQ ID NO: 1463.

Claim 85 (previously presented): The method of Claim 12, wherein determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell comprises determining whether said compound inhibits the growth of said sensitized cell to a greater extent than said compound inhibits the growth of said nonsensitized cell.

Claim 86 (previously presented): The method of Claim 12, wherein said prokaryotic organism is either *Staphylococcus aureus* or *Enteroccus faecalis*.

Claim 87 (previously presented): The method of Claim 86, wherein said prokaryotic organism is *Staphylococcus aureus* and said nucleotide sequence is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283.

Claim 88 (canceled):

Claim 89 (previously presented): The method of Claim 12, wherein said sensitized cell is a Gram positive bacterium.

Claim 90 (previously presented): The method of Claim 89, wherein said Gram positive bacterium is selected from the group consisting of *Staphylococcus* species, *Streptococcus* species, *Enterococcus* species, *Mycobacterium* species, *Clostridium* species, and *Bacillus* species.

Claim 91 (previously presented): The method of Claim 90, wherein said bacterium is *Staphylococcus aureus*.

Claim 92 (previously presented): The method of Claim 90, wherein said *Staphylococcus* species is coagulase negative.

Claim 93 (previously presented): The method of Claim 91, wherein said bacterium is selected from the group consisting of *Staphylococcus aureus* RN450 and *Staphylococcus aureus* RN4220.

Claim 94 (previously presented): The method of Claim 12, wherein said antisense nucleic acid is transcribed from an inducible promoter.

Claim 95 (previously presented): The method of Claim 12, further comprising the step of contacting said cell with a concentration of inducer which induces transcription of said antisense nucleic acid to a sublethal level.

Claim 96 (previously presented): The method of Claim 12, wherein growth inhibition is measured by monitoring optical density of a culture medium.

Claims 97-99 (canceled):

Claim 100 (previously presented): A method for screening a candidate compound for the ability to reduce cellular proliferation comprising the steps of:

(a) providing a sublethal level of an antisense nucleic acid selected from the group consisting of SEQ ID NOs: 521, 1390, 1463, 1845, 2782 and 3283, wherein said antisense nucleic acid reduces the activity or amount of a gene product required for cellular proliferation, thereby producing a sensitized cell, provided that said sensitized cell is a prokaryotic organism;

(b) contacting said sensitized cell with a compound; and

(c) determining the degree to which said compound inhibits proliferation of said sensitized cell relative to a nonsensitized cell.

Claim 101 (previously presented): The method of Claim 48, wherein said pathogenic mircoorganism is selected from the group consisting of *Anaplasma marginale, Aspergillus fumigatus, Bacillus anthracis, Bacterioides fragilis Bordetella pertussis, Burkholderia cepacia, Campylobacter jejuni, Candida albicans, Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis, Candida parapsilosis, Candida guilliermondii, Candida krusei, Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis, Chlamydia pneumoniae, Chlamydia trachomatus, Clostridium botulinum, Clostridium difficile, Clostridium perfringens, Coccidiodes immitis, Corynebacterium diptheriae, Cryptococcus neoformans, Enterobacter cloacae, Enterococcus faecalis, Enterococcus faecium, Escherichia coli, Haemophilus influenzae, Helicobacter pylori, Histoplasma capsulatum, Klebsiella pneumoniae, Listeria monocytogenes, Mycobacterium leprae, Mycobacterium tuberculosis, Neisseria gonorrhoeae, Neisseria meningitidis, Nocardia asteroides, Pasteurella haemolytica, Pasteurella multocida, Pneumocystis carinii, Proteus vulgaris, Pseudomonas aeruginosa, Salmonella bongori, Salmonella cholerasuis, Salmonella enterica, Salmonella paratyphi, Salmonella typhi, Salmonella typhimurium, Staphylococcus aureus, Listeria monocytogenes, Moxarella catarrhalis, Shigella boydii, Shigella dysenteriae, Shigella flexneri, Shigella sonnei,*

Staphylococcus epidermidis, Streptococcus pneumoniae, Streptococcus mutans, Treponema pallidum, Yersinia enterocolitica, Yersinia pestis and any species falling within the genera of any of the above species.

Claim 102 (canceled):

Claim 103 (previously presented): The method of Claim 100, wherein said prokaryotic organism is either *Staphylococcus aureus* or *Enteroccus faecalis*.

Claim 104 (previously presented): The method of Claim 103, wherein said prokaryotic organism is *Staphylococcus aureus* and said antisense nucleic acid is selected from the group consisting of SEQ ID NOs: 1390, 1463, 1845, 2782 and 3283.

Claim 105 (canceled).